IN THE CLAIMS:

1. (currently amended) An isolated nucleic acid encoding a peptide ~~consisting of about 21 to 40 amino acids~~ comprising a ZA loop of a bromodomain ~~comprising~~ wherein the ZA loop of the bromodomain comprises the amino acid sequence of SEQ ID NO:3.

2. (original) The isolated nucleic acid of Claim 1 further comprising a heterologous nucleotide sequence.

3. (original) An isolated nucleic acid encoding a peptide consisting of about 21 to 40 amino acids comprising a ZA loop of a bromodomain, wherein the bromodomain has an amino acid sequence selected from the group consisting of SEQ ID NOs. 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, and 42.

4. (original) The isolated nucleic acid of Claim 3 further comprising a heterogolous nucleotide sequence.

5. (original) A peptide consisting of about 21 to 40 amino acids comprising a ZA loop of a bromodomain comprising the amino acid sequence of SEQ ID NO:3.

6. (original) A fusion protein or peptide comprising the peptide of Claim 5.

7. (original) A peptide consisting of about 21 to 40 amino acids comprising a ZA loop of a bromodomain, wherein the bromodomain has an amino acid sequence selected from the group consisting of SEQ ID NOs. 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, and 42.

8. (original) A fusion protein or peptide comprising the peptide of Claim 7.

9. (original) An antibody raised against the peptide of Claim 7 or raised against an antigenic fragment thereof.

10. (original) An antibody raised against the peptide of Claim 5.

11. (original) A method of identifying a compound that modulates the affinity of a bromodomain for a ligand that comprises an acetyl-lysine, said method comprising:

(a) contacting the bromodomain and the ligand in the presence of the compound, wherein the bromodomain and the ligand bind in the absence of the compound; and

(b) measuring the affinity of the bromodomain for the ligand; wherein a compound is identified as a compound that modulates the affinity of the bromodomain for the ligand when there is a change in the affinity of the bromodomain for the ligand in the presence of the compound.

12. (original) The method of Claim 11, wherein the affinity of the bromodomain for the ligand increases in the presence of the compound and wherein the compound is identified as a bromodomain-ligand complex promoting agent.

13. (original) The method of Claim 11, wherein the affinity of the bromodomain for the ligand decreases in the presence of the compound and the compound is identified as an inhibitor.

14. (original) The method of Claim 11, wherein the compound is selected by performing rational drug design with the set of atomic coordinates obtained from one or more of Tables 1-6, wherein said selecting is performed in conjunction with computer modeling.

15. (original) The method of Claim 11, wherein the compound is selected by performing rational drug design with the set of atomic coordinates obtained from a set of atomic coordinates defining the three-dimensional structure of a bromodomain consisting of the amino acid sequence of SEQ ID NO:7, wherein said selecting is performed in conjunction with computer modeling.

16. (original) A method of identifying a compound that modulates the stability of a bromodomain-acetyl-lysine binding complex comprising:

(a) contacting the bromodomain-acetyl-lysine binding complex in the presence of the compound wherein the bromodomain-acetyl-lysine binding complex forms in the absence of the compound; and

(b) measuring the stability of the bromodomain-acetyl-lysine binding complex; wherein a compound is identified as a compound that modulates the stability of the bromodomain-acetyl-lysine binding complex, when there is a change in the stability of the bromodomain-acetyl-lysine binding complex in the presence of the compound.

17. (original) The method of Claim 16, wherein the stability of the bromodomain-acetyl-lysine binding complex increases in the presence of the compound and wherein the compound is identified as a stabilizing agent.

18. (original) The method of Claim 16, wherein the stability of the bromodomain-acetyl-lysine binding complex decreases in the presence of the compound and the compound is identified as an inhibitor.

19. (original) The method of Claim 16, wherein the compound is selected by performing rational drug design with the set of atomic coordinates obtained from one or more of Tables 1-6, wherein said selecting is performed in conjunction with computer modeling

20. (original) The method of Claim 16, wherein the compound is selected by performing rational drug design with the set of atomic coordinates obtained from a set of atomic coordinates defining the three-dimensional structure of a bromodomain consisting of the amino acid sequence of SEQ ID NO:7, wherein said selecting is performed in conjunction with computer modeling.

21. (currently amended) A method of identifying a binding partner for a protein that comprises an acetyl-lysine said method comprising:

(a) contacting the protein with a polypeptide comprising a bromodomain; and

(c b) determining whether the polypeptide binds to the protein; wherein a binding partner for a protein is identified when polypeptide binds to the protein.

22. (original) The method of Claim 21 wherein the brommodomain has an amino acid sequence selected from the group consisting of SEQ ID NOs. 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, and 42.

23. (original) An agent that can inhibit the binding of a bromodomain with a protein comprising an acetyl-lysine selected from the group consisting of: ISYGR-*AcK*-KRRQRR (SEQ ID NO:4), ARKSTGG-*AcK*-APRKQL (SEQ ID NO:5) and QSTSRHK-*AcK*-LMFKTE (SEQ ID NO:6).